

<110> Hoorn, Gert
Menke, Annette

<130> C10293us/JH/ml

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<210> 1

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<212> R.N.

<213> Influenza A virus

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 $\langle 220 \rangle$

<221> misc feature

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Modified influenza A 3'-sequence

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 $\langle 211 \rangle$ 12

<212> Rm.

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<223> Description of Artificial Sequence: Modified influenza A 3'-sequence

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<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified
influenza A 3'-sequence

ccugguucuc cu

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<213> Influenza A virus

aguagaaaca agg

13

<213> Influenza B virus

<223> n = any nucleotide

aguagwaaca rnn

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<213> Influenza C virus

agcaguagca agr

13

<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified influenza A 5'-sequence

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19

<210> 15
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acaaagtgtc gcccgagta ctggtcgacc tccgaagtgc ggggggagcg aaagcaggca 180

aaccatttga atg gat gtc aat ccg act tta ctg ttc ttg aaa gtt cct 229
Met Asn Val Asp Pro Thr I Lys Leu

Met	Asp	Val	Asn	Pro	Thr	Leu	Leu	Phe	Leu	Lys	Val	Pro
1				5					10			

gcg caa aat gca ata agt act acg ttc cct tac act gga gat cct cca 277

Ala Gly Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro

tac agc cat gga aca ggg aca gga tac acc atg gac aca gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Phe Val

Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
30 35 40 45

aca caa caa tat tgg gaa aag ggg aaa tgg aca aca aac act gag act 373
Thr His Glp Tyr Ser Glu Lys Glu Lys Phe Phe

Thr His Gln Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr
50 55 60

gga gca ccc caa ctt aat cca att gat ggc cca ttg cct gag gac aat 421

Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
65 70 75

gaa Glu	cca Pro	agt Ser 80	gga Gly	tat Tyr	gca Ala	caa Gln	aca Thr 85	gac Asp	tgc Cys	gtc Val	ctg Leu	gaa Glu 90	gca Ala	atg Met	gct Ala	469
ttc Phe	ctt Leu 95	gaa Glu	gaa Glu	tcc Ser	cat His	cca Pro 100	gga Gly	atc Ile	ttt Phe	gaa Glu	aac Asn 105	tcg Ser	tgt Cys	ctt Leu	gag Glu	517
acg Thr 110	atg Met	gaa Glu	gtt Val	gtt Val	caa Gln 115	caa Gln	aca Thr	aga Arg	gtg Val	gac Asp 120	aaa Lys	ctg Leu	acc Thr	caa Gln	ggc Gly 125	565
cgt Arg	cag Gln	act Thr	tat Tyr	gat Asp 130	tgg Trp	act Thr	ttg Leu	aat Asn 135	aga Arg	aac Asn	cag Gln	cct Pro	gct Ala	gca Ala 140	act Thr	613
gca Ala	tta Leu	gca Ala	aac Asn 145	act Thr	ata Ile	gag Glu	gtc Val	ttt Phe 150	aga Arg	tcg Ser	aat Asn	ggt Gly	cta Leu 155	aca Thr	gct Ala	661
aat Asn	gaa Glu	tca Ser 160	ggg Gly	agg Arg	ctc Leu	ata Ile	gat Asp 165	ttc Phe	ctc Leu	aag Lys	gat Asp 170	gtg Val	atg Met	gaa Glu	tca Ser	709
atg Met	gat Asp 175	aag Lys	gag Glu	gaa Glu	atg Met	gag Glu 180	ata Ile	aca Thr	aca Thr	cat His	ttc Phe 185	caa Gln	cga Arg	aag Lys	aga Arg	757
aga Arg 190	gta Val	aga Arg	gac Asp	aac Asn	atg Met 195	acc Thr	aag Lys	aaa Lys	atg Met	gtc Val 200	aca Thr	caa Gln	aga Arg	aca Thr	ata Ile 205	805
ggg Gly	aag Lys	aaa Lys	aag Lys	cag Gln 210	aga Arg	ctt Leu	aac Asn	aaa Lys	agg Arg 215	agc Ser	tac Tyr	cta Leu	ata Ile	agg Arg 220	gct Ala	853
cta Leu	aca Thr	ttg Leu	aac Asn 225	aca Thr	atg Met	acg Thr	aaa Lys	gat Asp 230	gca Ala	gaa Glu	aga Arg	ggt Gly	aaa Lys 235	ctg Leu	aag Lys	901
aga Arg	aga Arg	gca Ala 240	att Ile	gca Ala	aca Thr	cca Pro	ggg Gly 245	atg Met	cag Gln	atc Ile	aga Arg	ggg Gly 250	ttt Phe	gtg Val	tac Tyr	949
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ggg Gly 270	cta Leu	cca Pro	gtt Val	gga Gly	ggg Gly 275	aat Asn	gag Glu	aag Lys	aaa Lys	gct Ala 280	aaa Lys	ttg Leu	gca Ala	aat Asn	gtc Val 285	1045
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aga Arg	aat Asn 335	gtc Val	ttg Leu	agc Ser	atc Ile	gcg Ala 340	ccg Pro	ata Ile	atg Met	ttt Phe	tcg Ser 345	aac Asn	aaa Lys	atg Met	gcg Ala	1237

agg cta ggg aaa ggg tac atg ttc gaa agc aaa agc atg aag ctc cga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg
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aca caa ata cca gca gaa atg cta gca agt att gat cta aaa tat ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata 1381
 Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile
 385 390 395

gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn
 400 405 410

atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys
 415 420 425

aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat 1525
 Arg Tyr Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp
 430 435 440 445

gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala
 450 455 460

gga gtg gat aga ttc tac aga acc tgc aag cta gtt ggg atc aat atg 1621
 Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met
 465 470 475

agc aag aaa aag tcc tat ata aat agg aca gga aca ttc gaa ttc aca 1669
 Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr
 480 485 490

agc ttt ttc tac cgc tat gga ttt gta gcc aat ttt agt atg gag ttg 1717
 Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu
 495 500 505

ccc agc ttt gga gta tca gga att aat gaa tcg gct gat atg agc att 1765
 Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile
 510 515 520 525

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 Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro
 530 535 540

gca aca gcc caa atg gct ctc caa tta ttc atc aag gac tac aga tat 1861
 Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr
 545 550 555

aca tac agg tgt cac agg gga gac aca caa atc caa acg agg agg tca 1909
 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser
 560 565 570

ttc gag cta aag aag ctg tgg gag cag acc cgc tca aag gca gga ctg 1957
 Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu
 575 580 585

ttg gtt tca gat ggc gga cca aac ctg tac aac att cgg aat ctc cac 2005
 Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His
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1007-0000

atc ccg gaa gtt tgc ctg aaa tgg gaa cta atg gat gaa gac tat cag 2053
 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln
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 Gly Arg Leu Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile
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gaa tct gta aac aat gct gcg gta atg cca gcc cat ggt cca gcc aaa 2149
 Glu Ser Val Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys
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agc atg gaa tat gat gct gtg gca act aca cac tct tgg atc cct aag 2197
 Ser Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
 655 660 665

aga aac cgt tcc att ctc aat acg agt caa agg gga atc ctt gag gat 2245
 Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp
 670 675 680 685

gaa caa atg tac cag aag tgt tgc aac cta ttc gag aaa ttc ttc cct 2293
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 720 725 730

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 Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745

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<223> Description of Artificial Sequence: FPV-Br.-PB1

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35 40 45

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80

Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu
100 105 110

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asp Lys
165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys
195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
225 230 235 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
260 265 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
275 280 285

Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
290 295 300

Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
305 310 315 320

Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
325 330 335

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Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	Asn	Glu	Pro	
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Gly	Val	Ser	Gly	Ile	Asn	Glu	Ser	Ala	Asp	Met	Ser	Ile	Gly	Val	Thr	
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Gln	Met	Ala	Leu	Gln	Leu	Phe	Ile	Lys	Asp	Tyr	Arg	Tyr	Thr	Tyr	Arg	
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Val	Cys	Leu	Lys	Trp	Glu	Leu	Met	Asp	Glu	Asp	Tyr	Gln	Gly	Arg	Leu	
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Cys	Asn	Pro	Met	Asn	Pro	Phe	Val	Ser	His	Lys	Glu	Ile	Glu	Ser	Val	
625					630					635					640	
Asn	Asn	Ala	Ala	Val	Met	Pro	Ala	His	Gly	Pro	Ala	Lys	Ser	Met	Glu	
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Ser	Ile	Leu	Asn	Thr	Ser	G										

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala	
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Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys	
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Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
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Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
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Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
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Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
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20030220 "ZEE" 0001

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Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
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Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
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aga Arg 670	aat Asn	cga Arg	tcc Ser	atc Ile	ttg Leu 675	aat Asn	aca Thr	agc Ser	caa Gln	aga Arg 680	gga Gly	ata Ile	ctt Leu	gaa Glu	gat Asp 685	2245
gaa Glu	caa Gln	atg Met	tac Tyr	caa Gln 690	aag Lys	tgc Cys	tgc Cys	aac Asn	tta Leu 695	ttt Phe	gaa Glu	aaa Lys	ttc Phe	ttc Phe 700	ccc Pro	2293
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atg Met	gtt Val	tcc Ser 720	aga Arg	gcc Ala	cga Arg	att Ile	gat Asp 725	gca Ala	cga Arg	att Ile	gat Asp	ttc Phe 730	gaa Glu	tct Ser	gga Gly	2389
agg Arg	ata Ile 735	aag Lys	aaa Lys	gag Glu	gag Glu	ttc Phe 740	act Thr	gag Glu	atc Ile	atg Met	aag Lys 745	atc Ile	tgt Cys	tcc Ser	acc Thr	2437

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 35 40 45
 Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60
 Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80
 Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95
 Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu
 100 105 110
 Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125
 Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
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 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asp Lys
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1007337.020302

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
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 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys
 195 200 205
 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
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 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
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 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp
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 Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
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 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
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 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
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100237 020809
 200809 200809

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
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Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
545 550 555 560

Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
565 570 575

Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
580 585 590

Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
610 615 620

Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
625 630 635 640

Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
645 650 655

Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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	Met	Asp	Val	Asn	Pro	Thr	Leu	Leu	Phe	Leu	Lys	Val	Pro			
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Ala	Gln	Asn	Ala	Ile	Ser	Thr	Thr	Phe	Pro	Tyr	Thr	Gly	Asp	Pro	Pro	
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tac	agc	cat	ggg	aca	gga	aca	gga	tac	acc	atg	gat	act	gtc	aac	agg	325
Tyr	Ser	His	Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	Thr	Val	Asn	Arg	
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Thr	His	Gln	Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	
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gga	gca	ccg	caa	ctc	aac	ccg	att	gat	ggg	cca	ctg	cca	gaa	gac	aat	421
Gly	Ala	Pro	Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	
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gaa	cca	agt	ggg	tat	gcc	caa	aca	gat	tgt	gta	ttg	gaa	gca	atg	gcc	469
Glu	Pro	Ser	Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	
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ttc	ctt	gag	gaa	tcc	cat	cct	ggg	atc	ttt	gag	acc	tcg	tgt	ctt	gaa	517
Phe	Leu	Glu	Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	
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acg	atg	gag	gtt	gtt	cag	caa	aca	cga	gtg	gac	aag	ctg	aca	caa	ggc	565
Thr	Met	Glu	Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	
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cga	cag	acc	tat	gac	tgg	act	cta	aat	agg	aac	cag	cct	gct	gca	aca	613
Arg	Gln	Thr	Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	
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Ala	Leu	Ala	Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	
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Asn	Glu	Ser	Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	
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Met	Asn	Lys	Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	
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Arg	Val	Arg	Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	
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Gly	Lys	Arg	Lys</													

ggg cta cca gtt gga ggg aat gag aag aaa gct aaa ttg gca aat gtc 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val 285
 270 275 280

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 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr 300
 290 295

atc acc gga gac aat acc aaa tgg aat gag aac caa aac ccc cga atg 1141
 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met 315
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ttc ctg gca atg ata aca tac atc aca aga aac caa cct gag tgg ttt 1189
 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe 330
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aga aat gtc ttg agc atc gcg ccg ata atg ttt tcg aac aaa atg gcg 1237
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 335 340

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 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg 365
 350 355 360

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 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe 380
 370 375

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata 1381
 Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile 395
 385 390

gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn 410
 400 405

atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys 425
 415 420

aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat 1525
 Arg Tyr Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp 445
 430 435 440

gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala 460
 450 455

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 465 470

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 Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr 490
 480 485

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 495 500

ccc agc ttt gga gta tca gga att aat gaa tcg gct gat atg agc att 1765
 Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile 525
 510 515 520

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<223> Description of Artificial Sequence: pHL3130
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          35          40          45
Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
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Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
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Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
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Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
          100          105          110
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Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
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Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
          145          150          155          160
Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
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Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
          180          185          190
Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
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Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
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 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
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 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
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 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
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 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
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 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr
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 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp
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 Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
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 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
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 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
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 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
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 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
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 625 630 635 640
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 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
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 acaaagtgtc gcccgagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
 aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
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 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
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Gly	Ala	Pro	Gln 65	Leu	Asn	Pro	Ile	Asp 70	Gly	Pro	Leu	Pro	Glu 75	Asp	Asn	
gaa	cca	agt	ggt	tat	gcc	caa	aca	gat	tgt	gta	ttg	gaa	gca	atg	gcc	469
Glu	Pro	Ser 80	Gly	Tyr	Ala	Gln	Thr 85	Asp	Cys	Val	Leu	Glu 90	Ala	Met	Ala	
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Phe	Leu 95	Glu	Glu	Ser	His	Pro 100	Gly	Ile	Phe	Glu	Thr 105	Ser	Cys	Leu	Glu	
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Thr 110	Met	Glu	Val	Val	Gln 115	Gln	Thr	Arg	Val	Asp 120	Lys	Leu	Thr	Gln 125	Gly	
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Arg	Gln	Thr	Tyr	Asp 130	Trp	Thr	Leu	Asn 135	Arg	Asn	Gln	Pro	Ala	Ala 140	Thr	
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Met	Asn 175	Lys	Glu	Glu	Met	Glu 180	Ile	Thr	Thr	His	Phe 185	Gln	Arg	Lys	Arg	
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Val	Arg	Lys	Met	Met 290	Thr	Asn	Ser	Gln	Asp 295	Thr	Glu	Leu	Ser 300	Phe	Thr	

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 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe
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 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
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 Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
 655 660 665

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 670 675 680 685

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 720 725 730

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 735 740 745

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 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: pHL3131

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Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	Thr	Val	Asn	Arg	Thr	His	Gln	35	40	45	
Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	Gly	Ala	Pro	50	55	60	
Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	Glu	Pro	Ser	65	70	75	80
Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	Phe	Leu	Glu	85	90	95	
Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	Thr	Met	Glu	100	105	110	
Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr	115	120	125	
Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	Ala	Leu	Ala	130	135	140	
Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	Asn	Glu	Ser	145	150	155	160
Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	Met	Asn	Lys	165	170	175	
Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	Arg	Val	Arg	180	185	190	
Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Arg	195	200	205	
Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu	210	215	220	
Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	Arg	Arg	Ala	225	230	235	240
Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu	245	250	255	
Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	Gly	Leu	Pro	260	265	270	
Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	Val	Arg	Lys	275	280	285	

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 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
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 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
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 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr
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 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
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 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
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 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
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aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
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Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
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Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
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 Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
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aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg
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act caa ata cct gca gaa atg cta gca agc atc gat ttg aaa tac ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
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aat gat tca act aga aag aag att gaa aaa atc cgg ccg ctc tta ata 1381
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aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa	2197
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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
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Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
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Val	Val	Gln 115	Gln	Thr	Arg	Val	Asp 120	Lys	Leu	Thr	Gln	Gly 125	Arg	Gln	Thr
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Gly	Arg	Leu	Ile 165	Asp	Phe	Leu	Lys	Asp	Val 170	Met	Glu	Ser	Met	Asn 175	Lys
Glu	Glu	Met	Glu 180	Ile	Thr	Thr	His	Phe 185	Gln	Arg	Lys	Arg	Arg 190	Val	Arg
Asp	Asn 195	Met	Thr	Lys	Lys	Met	Val 200	Thr	Gln	Arg	Thr	Ile 205	Gly	Lys	Arg
Lys	Gln 210	Arg	Leu	Asn	Lys	Arg 215	Ser	Tyr	Leu	Ile	Arg 220	Ala	Leu	Thr	Leu
Asn 225	Thr	Met	Thr	Lys	Asp 230	Ala	Glu	Arg	Gly	Lys 235	Leu	Lys	Arg	Arg	Ala 240
Ile	Ala	Thr	Pro	Gly 245	Met	Gln	Ile	Arg	Gly 250	Phe	Val	Tyr	Phe	Val 255	Glu
Thr	Leu	Ala	Arg 260	Ser	Ile	Cys	Glu	Lys 265	Leu	Glu	Gln	Ser	Gly 270	Leu	Pro
Val	Gly 275	Gly	Asn	Glu	Lys	Lys	Ala 280	Lys	Leu	Ala	Asn	Val 285	Val	Arg	Lys
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Asp 305	Asn	Thr	Lys	Trp	Asn 310	Glu	Asn	Gln	Asn	Pro 315	Arg	Met	Phe	Leu	Ala 320
Met	Ile	Thr	Tyr 325	Ile	Thr	Arg	Asn	Gln	Pro 330	Glu	Trp	Phe	Arg	Asn 335	Val
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Lys	Gly 355	Tyr	Met	Phe	Glu	Ser	Lys 360	Ser	Met	Lys	Ile	Arg 365	Thr	Gln	Ile
Pro 370	Ala	Glu	Met	Leu	Ala	Ser 375	Ile	Asp	Leu	Lys	Tyr 380	Phe	Asn	Asp	Ser
Thr 385	Arg	Lys	Lys	Ile	Glu 390	Lys	Ile	Arg	Pro	Leu 395	Leu	Ile	Asp	Gly	Thr 400
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AACCATTGTA	ATG	GAT	GTC	AAT	CCG	ACT	TTA	CTT	TTC	TTA	AAA	GTG	CCA	229						
	Met	Asp	Val	Asn	Pro	Thr	Leu	Leu	Phe	Leu	Lys	Val	Pro	.						
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GCA	CAA	AAT	GCT	ATA	AGC	ACA	ACT	TTC	CCT	TAT	ACT	GGA	GAC	CCT	CCT	277				
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Arg	Gln	Thr	Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr					
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Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
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  100              105              110
Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
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Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	Arg	Val	Arg
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Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	Lys	Leu	Arg	Thr	Gln	Ile
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Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	Asn	Asp	Ser
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Lys	Thr	Thr	Tyr	Trp	Trp	Asp	Gly	Leu	Gln	Ser	Ser	Asp	Asp	Phe	Ala
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 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
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 625 630 635 640
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 645 650 655
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 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
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 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
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 Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
 65 70 75
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 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
 80 85 90
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 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
 95 100 105
 acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
 Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
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 Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
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 Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
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 Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
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 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr
 290 295 300

atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg 1141
 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met
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 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg
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 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

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 Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile
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 415 420 425

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 Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile
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 545 550 555

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 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser
 560 565 570

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 Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu
 575 580 585

ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac 2005
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 590 595 600 605

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 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln
 610 615 620

ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att 2101
 Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile
 625 630 635

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 Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys
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 670 675 680 685

gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc 2293
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 690 695 700

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 Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60
 Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80
 Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95
 Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
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 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175
 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190

Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Arg	
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Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu	
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Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu	
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Ala	Ser	Leu	Ser	Pro	Gly	Met	Met	Met	Gly	Met	Phe	Asn	Met	Leu	Ser	
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Tyr	Arg	Tyr	Gly	Phe	Val	Ala	Asn	Phe	Ser	Met	Glu	Leu	Pro	Ser	Phe	
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Val	Ile	Lys	Asn	Asn	Met	Ile	Asn</									

Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
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 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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 <222> (191)..(2461)

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 acaaagtgtc gcccgagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
 aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
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208020-03000

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cga Arg	gtg Val	aga Arg	gac Asp	aat Asn	atg Met	act Thr	aag Lys	aaa Lys	atg Met	gtg Val	aca Thr	cag Gln	aga Arg	aca Thr	ata Ile	805
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225230235																
cgg Arg	aga Arg	gca Ala	att Ile	gca Ala	acc Thr	cca Pro	ggg Gly	atg Met	caa Gln	ata Ile	agg Arg	ggg Gly	ttt Phe	gta Val	tac Tyr	949
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gta Val	agg Arg	aag Lys	atg Met	atg Met 290	acc Thr	aat Asn	tct Ser	cag Gln	gac Asp 295	act Thr	gaa Glu	att Ile	tct Ser	ttc Phe 300	acc Thr	1093
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aga Arg 350	ctg Leu	gga Gly	aag Lys	ggg Gly 355	tac Tyr	atg Met	ttt Phe	gag Glu	agc Ser 360	aag Lys	agt Ser	atg Met	aaa Lys	att Ile	aga Arg 365	1285
act Thr	caa Gln	ata Ile	cct Pro	gca Ala 370	gaa Glu	atg Met	cta Leu	gca Ala 375	agt Ser	att Ile	gat Asp	cta Leu	aaa Lys	tat Tyr 380	ttc Phe	1333
aat Asn	gaa Glu	cca Pro	aca Thr 385	agg Arg	aag Lys	aaa Lys	atc Ile	gag Glu 390	aaa Lys	ata Ile	agg Arg	cct Pro	ctc Leu 395	tta Leu	ata Ile	1381
gat Asp	ggg Gly	act Thr 400	gca Ala	tca Ser	ttg Leu	agc Ser	cct Pro 405	gga Gly	atg Met	atg Met	atg Met	ggc Gly 410	atg Met	ttc Phe	aat Asn	1429
atg Met	tta Leu 415	agt Ser	act Thr	gta Val	tta Leu	ggc Gly 420	gtc Val	tcc Ser	atc Ile	ctg Leu	aat Asn 425	ctt Leu	gga Gly	caa Gln	aag Lys	1477
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gat Asp	ttt Phe	gct Ala	ctg Leu	att Ile 450	gtg Val	aat Asn	gca Ala	ccc Pro	aat Asn 455	cat His	gaa Glu	ggg Gly	att Ile	caa Gln 460	gcc Ala	1573
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ccc Pro 510	agc Ser	ttt Phe	ggg Gly	gtg Val	tct Ser 515	ggg Gly	atc Ile	aac Asn	gag Glu	tct Ser 520	gcg Ala	gac Asp	atg Met	agt Ser	att Ile 525	1765
gga Gly	gtt Val	act Thr	gtc Val	atc Ile 530	aaa Lys	aac Asn	aat Asn	atg Met	ata Ile 535	aac Asn	aat Asn	gat Asp	ctt Leu	ggg Gly 540	cca Pro	1813
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3571
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 3751
 3811
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Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	Thr	Val	Asn	Arg	Thr	His	Gln	
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Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	Gly	Ala	Pro	
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Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	Glu	Pro	Ser	
65					70					75					80	
Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	Phe	Leu	Glu	
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Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	Thr	Met	Glu	
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Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr	
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 290 295 300
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 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
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 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
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 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
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<222> (191)..(2461)
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aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
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gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
      15              20              25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
      30              35              40              45

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Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
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gaa Glu	cca Pro	agt Ser 80	ggt Gly	tat Tyr	gcc Ala	caa Gln	aca Thr 85	gat Asp	tgt Cys	gta Val	ttg Leu 90	gaa Glu 90	gca Ala	atg Met	gcc Ala	469
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acg Thr 110	atg Met	gag Glu	ggt Val	gtt Val	cag Gln 115	caa Gln	aca Thr	cga Arg	gtg Val	gac Asp 120	aag Lys	ctg Leu	aca Thr	caa Gln	ggc Gly 125	565
cga Arg	cag Gln	acc Thr	tat Tyr	gac Asp 130	tgg Trp	act Thr	cta Leu	aat Asn	agg Arg 135	aac Asn	cag Gln	cct Pro	gct Ala	gca Ala 140	aca Thr	613
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Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
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Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
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